

RAW SEQUENCE LISTING

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Application Serial Number: 10/736,868

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PATENT APPLICATION: US/10/736,868

DATE: 12/22/2004

TIME: 15:26:10

Input Set : A:\08451~1.txt

Output Set: N:\CRF4\12222004\J736868.raw

3 <110> APPLICANT: Solomon, Aaron
 4 Morimoto, Richard
 5 Beitel, Greg
 7 <120> TITLE OF INVENTION: OSR-1 Nucleic Acids and Proteins
 9 <130> FILE REFERENCE: NWESTERN-08451
 11 <140> CURRENT APPLICATION NUMBER: 10/736,868
 12 <141> CURRENT FILING DATE: 2003-12-16
 14 <160> NUMBER OF SEQ ID NOS: 6
 16 <170> SOFTWARE: PatentIn version 3.2
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 1932
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Caenorhabditis elegans
 23 <400> SEQUENCE: 1

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28	catcaaaaac	taccactggc	tccatcaatg	gaagctttg	aactgtatgg	tgttcaattt	180
30	gttgatgctc	tcatcaaaaa	aggtaaaatg	gaaatggcaa	aaggagcatt	taagactcaa	240
32	ttagaagttc	tagagaaaatg	acatcctgtat	caattcgata	agtacaaaaaa	gctaaaagtt	300
34	gatgatttgg	cagctgtatgc	agttatgcaa	caggcggaga	tggcaaaatt	acagcctaaa	360
36	tcagggaaatg	catttatcga	tatgttgaat	ggaaatggaa	tcccaattgg	tagcagtatt	420
38	cgtggattag	aagatgtat	ccgaacgcag	agagatatgg	aaaatacggaa	tccgtccgaa	480
40	cagattgcca	aagccgtaat	ggacaaattt	caaacacaaa	ttctcccagg	actcggtgca	540
42	aatatgatcg	ctggcaagaa	ccccttaaa	atgcctcaac	aaatgagaaa	agctcaagct	600
44	gctccatcg	cagtgttcca	acaagcttt	gctcaaagag	caatgtttagg	taaaaatgcc	660
46	ccagttgccg	gtggaaagagg	tgaagaacaa	cggatgtat	tgaatcgagt	ggaccaaaga	720
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54	gttcaatcat	tgctcttta	ccaaacgaatg	agggatttcc	cactgagcaa	gcgaaggcct	960
56	ttggctatga	acgatgagga	tgaaagtgc	ttccgcgcaa	tggaggctcg	tgc当地acta	1020
58	gatcaaaaat	ctcaacttgt	gctcggcttc	catggtttt	gagagtctga	tgtatgtgaa	1080
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62	cgtctttctt	ccggattctgt	tgagaaattt	aagtcaatg	atgaattgaa	aagtgcattt	1200
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74	atgttaactg	atgaaacagaa	aggttagaaca	cgtgtcaaaa	caattcgat	attaccaaga	1560
76	ctgttcgggt	caccaactgc	aaaagctgaa	atgattgtat	caaaggattt	ccaagatatt	1620
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80	tggactggag	caaataaaaa	agaaattccaa	ggacttggaa	gtcgatccat	tctccatct	1740

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82 cttgatccaa ctatgccagc cttgaacacg gctttctcga ctcagggcgc agcccggtgac 1800
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 106 Leu Ser Ser Leu Val Gly Lys Ser His Gln Lys Leu Pro Leu Ala Pro
 107 35 40 45
 110 Ser Met Glu Ala Leu Glu Leu Met Gly Val Gln Phe Val Asp Ala Leu
 111 50 55 60
 114 Ile Lys Lys Gly Gln Met Glu Met Ala Lys Gly Ala Phe Lys Thr Gln
 115 65 70 75 80
 118 Leu Glu Val Leu Glu Lys Val His Pro Asp Gln Phe Asp Lys Tyr Lys
 119 85 90 95
 122 Lys Leu Lys Val Asp Asp Leu Ala Ala Asp Ala Val Met Gln Gln Ala
 123 100 105 110
 126 Glu Met Ala Lys Leu Gln Pro Lys Ser Gly Asn Ala Phe Ile Asp Met
 127 115 120 125
 130 Leu Asn Gly Asn Gly Ile Pro Ile Gly Ser Ser Ile Arg Gly Leu Glu
 131 130 135 140
 134 Asp Ala Ile Arg Thr Gln Arg Asp Met Glu Asn Thr Asp Pro Ser Glu
 135 145 150 155 160
 138 Gln Ile Ala Lys Ala Val Met Asp Lys Phe Gln Thr Gln Ile Leu Pro
 139 165 170 175
 142 Gly Leu Val Ala Asn Met Ile Ala Gly Lys Asn Pro Phe Lys Met Pro
 143 180 185 190
 146 Gln Gln Met Arg Lys Ala Gln Ala Ala Pro Ser Ser Val Phe Gln Gln
 147 195 200 205
 150 Ala Leu Ala Gln Arg Ala Met Leu Gly Lys Asn Ala Pro Val Ala Gly
 151 210 215 220
 154 Gly Arg Gly Glu Glu Gln Arg Met Met Met Asn Arg Val Asp Gln Arg
 155 225 230 235 240
 158 Met Gln Gln Arg Glu Leu Gln Glu Asp Glu Asp Asp Asp Asp Leu
 159 245 250 255
 162 Glu Asp Glu Asp Val Pro Arg Arg Ser Ser Asp Gly Glu Pro Gln
 163 260 265 270
 166 Ser Glu Ala Glu His Gln Arg Arg Asp Leu Ala Arg Arg Leu Lys Ser
 167 275 280 285
 170 Ser Pro Arg Leu Lys Glu Leu Leu Gln Asn Ala Glu Val Gln Ser Leu
 171 290 295 300
 174 Leu Ser Tyr Gln Arg Met Arg Asp Ser Pro Leu Ser Lys Arg Arg Pro
 175 305 310 315 320

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 179 325 330 335
 182 Arg Ala Lys Leu Asp Gln Lys Ser Gln Leu Val Leu Gly Leu His Gly
 183 340 345 350
 186 Phe Gly Glu Ser Asp Asp Asp Glu Asp Glu Asp Glu Asn Leu Ile
 187 355 360 365
 190 Asp Pro Ser Glu Asn Ser Phe Arg Arg Ala Pro Leu Arg Leu Ser Ser
 191 370 375 380
 194 Gly Phe Val Glu Lys Leu Lys Ser Asn Asp Glu Leu Lys Ser Ala Leu
 195 385 390 395 400
 198 Asp Arg Ile Lys Tyr Arg Val Asp Asp Val Glu Lys Tyr Leu Ala Pro
 199 405 410 415
 202 Lys Pro Met Glu Phe Asn Pro Lys Pro Gln Pro Gly Tyr Phe Ala Pro
 203 420 425 430
 206 Arg Lys Ile Pro Thr Arg Pro Arg Lys Met Leu Pro Leu Leu Ile Gly
 207 435 440 445
 210 Ser Asp Pro Lys Val Gln Glu Glu Ile Arg Arg His Pro Ser Thr Glu
 211 450 455 460
 214 Trp Lys Ile Ala Lys Glu Ser Arg Val Leu Thr Asn Leu Lys Asn Asn
 215 465 470 475 480
 218 Pro Ser Leu Ala Ala Leu Phe Met Asp Asp Lys Leu Glu Asn Thr Leu
 219 485 490 495
 222 Lys Gly Arg Gln Met Leu Thr Asp Glu Gln Lys Gly Arg Thr Arg Val
 223 500 505 510
 226 Lys Thr Ile Arg Ala Leu Pro Arg Leu Phe Gly Ala Pro Thr Ala Lys
 227 515 520 525
 230 Ala Glu Met Ile Asp Ala Lys Val Phe Gln Asp Ile Glu Glu Arg Pro
 231 530 535 540
 234 Ile Pro Pro Leu Phe Phe Glu Pro Lys Gly Arg His Thr Arg Leu Arg
 235 545 550 555 560
 238 Trp Thr Gly Ala Asn Glu Lys Glu Ile Pro Gly Leu Gly Ser Arg Phe
 239 565 570 575
 242 Ile Leu Pro Ser Leu Asp Pro Thr Met Pro Ala Leu Asn Thr Ala Phe
 243 580 585 590
 246 Ser Thr Gln Gly Arg Ala Arg Asp Glu Trp Asp Thr Met Phe Lys Ile
 247 595 600 605
 250 Pro Asn Asn Trp Asn Pro Gly Asp Glu Val Gly Phe Lys Met Asn Ser
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 265 <213> ORGANISM: Caenorhabditis elegans
 267 <400> SEQUENCE: 3
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 272 cgtccgctac tactgtatct tctggacatc tacctgtata cacaccagtg gccagtcatc 180

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326	tgtggatac	tatggatgtt	gatgcattga	tcagacatga	gctgagtcaa	gctggagggc	1800
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336	ctttctctcg	tctaatttca	acacattat	cccagtgc	tcgtgtata	ataatataaa	2100
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371 <212> TYPE: PRT
372 <213> ORGANISM: *Caenorhabditis elegans*
374 <400> SEQUENCE: 4
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385 35 40 45
388 Met His Pro His His Gln Leu Pro His Met Gln Gln Leu Pro Gln Pro
389 50 55 60
392 Leu Leu Asn Leu Asn Met Thr Thr Leu Thr Ser Ser Gly Ser Ser Val
393 65 70 75 80
396 Ala Ser Ser Ile Gly Gly Gly Ala Gln Cys Ser Pro Cys Ala Ser Gly
397 85 90 95
400 Ser Ser Thr Ala Ala Thr Asn Ser Ser Gln Gln Gln Thr Val Gly
401 100 105 110
404 Gln Met Leu Ala Ala Ser Val Pro Cys Ser Ser Gly Met Thr Leu
405 115 120 125
408 Gly Met Ser Leu Asn Leu Ser Gln Gly Gly Pro Met Pro Ala Lys
409 130 135 140
412 Lys Lys Arg Cys Arg Lys Lys Pro Thr Asp Gln Leu Ala Gln Lys Lys
413 145 150 155 160
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417 165 170 175
420 Leu Glu Ser Ala Pro Asp Gly Arg Leu Lys Leu Asn Glu Ile Tyr Gln
421 180 185 190
424 Trp Phe Ser Asp Asn Ile Pro Tyr Phe Gly Glu Arg Ser Ser Pro Glu
425 195 200 205
428 Glu Ala Ala Gly Trp Lys Asn Ser Ile Arg His Asn Leu Ser Leu His
429 210 215 220
432 Ser Arg Phe Met Arg Ile Gln Asn Glu Gly Ala Gly Lys Ser Ser Trp
433 225 230 235 240
436 Trp Val Ile Asn Pro Asp Ala Lys Pro Gly Arg Asn Pro Arg Arg Thr
437 245 250 255
440 Arg Glu Arg Ser Asn Thr Ile Glu Thr Thr Thr Lys Ala Gln Leu Glu
441 260 265 270
444 Lys Ser Arg Arg Gly Ala Lys Lys Arg Ile Lys Glu Arg Ala Leu Met
445 275 280 285
448 Gly Ser Leu His Ser Thr Leu Asn Gly Asn Ser Ile Ala Gly Ser Ile
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452 Gln Thr Ile Ser His Asp Leu Tyr Asp Asp Asp Ser Met Gln Gly Ala
453 305 310 315 320
456 Phe Asp Asn Val Pro Ser Ser Phe Arg Pro Arg Thr Gln Ser Asn Leu
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464 Ile Tyr Asp Asp Leu Glu Phe Pro Ser Trp Val Gly Glu Ser Val Pro
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VERIFICATION SUMMARY

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